

MAY. 1. 2002 5:38PM

TTC PALO ALTO **AA alignment** ~~ext~~

NO. 1073 P. 30

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DIALIGN 2.1

m, Kornelia Frech,
ress Klaus Hahn, Thomas Werner, Jens Stoye, Andreas D

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cite: Published research assisted by DIALIGN 2 should

ent B. Morgenstern (1999),
"DIALIGN 2: improvement of the segment-to-segment
approach to multiple sequence alignment."
Bioinformatics 15, 203 - 210.

Options:

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- 1) protein sequences aligned
- 2) 5 "*" characters for regions of maximum similarity

Aligned sequences:

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length:

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1)	855444	501
2)	2	501

Average sequence length: 501.000

Please note that only upper-case letters are considered to be aligned.

For more information, have a look at the user guide

http://bibiserv.techfak.uni-bielefeld.de/dialign/user_guide

ide2.html

Alignment (DIALIGN format):
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855444 1 MAQALPWLLL WMGAGVLPAH GTQHGIPLPL RSGLGGAPL
G LRLPRETDEE
2 1 MAQALPWLLL WMGAGVLPAH GTQHGIPLPL RSGLGGAPL
G LRLPRETDEE

* *****
* *****
* *****
* *****
* *****
* *****

855444 51 PEEPGRGSF VEMVDNLRGK SGQGYYVEMT VGSPPQTLN
I LVDTGSSNFA
2 51 PEEPGRGSF VEMVDNLRGK SGQGYYVEMT VGSPPQTLN
I LVDTGSSNFA

* *****
* *****
* *****
* *****
* *****

855444 101 VGAAPHFPLH RYYQRQLSST YRDLRKGVYE PYTQGKWE^G
E LGTDLVSI^H
2 101 VGAAPHFPLH RYYQRQLSST YRDLRKGVY^V PYTQGKWE^G
E LGTDLVSI^H

* *****
* *****
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* *****
* *****
* *****

855444 151 GPNVTVRANI AAITESDKFF INGSNWEGL GLAYAEIAR
P DDSLEPFFDS
2 151 GPNVTVRANI AAITESDKFF INGSNWEGL GLAYAEIAR
P DDSLEPFFDS

* *****
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* *****
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* *****

855444 201 LVKQTHVPNL FSLQLCGAGF PLNQSEVLAS VGGSMIIGG
I DHSLYTGSLW
2 201 LVKQTHVPNL FSLQLCGAGF PLNQSEVLAS VGGSMIIGG
I DHSLYTGSLW

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855444 251 YTPIRREWYY EVIIVRVEIN GQDLKMDCKE YNYDKSIVD
S GTTNLRLPKK
2 251 YTPIRREWYY EVIIVRVEIN GQDLKMDCKE YNYDKSIVD
S GTTNLRLPKK

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* *****
* *****

855444 301 VFEAAVKSIAK AASSTEKFDP GFWLGEQLVC WQAGTTPWN
I FPVISLYLMG
2 301 VFEAAVKSIAK AASSTEKFDP GFWLGEQLVC WQAGTTPWN
I FPVISLYLMG

* *****
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* *****
* *****
* *****

855444 351 EVTNQSFRIT ILPOQYLRPV EDVATSQDDC YKFAISQSS
T GTVMGAVIME

2
T GTVMGAVIME

351

EVTNQSFRIT ILPQQYLRPV EDVATSQDDC YKFAISQSS

* *****
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* *****
* *****
* *****
* **********

*****855444 401
M EDCGYNIPQT
2 401
M EDCGYNIPQTGFYVVFDRAR KRIGFAVSAC HVHDEFRTAA VEGPFVTLD
GFYVVFDRAR KRIGFAVSAC HVHDEFRTAA VEGPFVTLD* *****
* *****
* *****
* *****
* *****
* **********

*****855444 451
H DDFADDISLL
2 451
H DDFADDISLLDESTLMTIAY VMAAICALFM LPLCLMVCQW RCLRCLRQQ
DESTLMTIAY VMAAICALFM LPLCLMVCQW RCLRCLRQQ* *****
* *****
* **********

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* *****

855444

2

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Alignment (FASTA format):

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>855444

MAQALPWLLLWMGAGVLP AHLTQH GIRLPLRSGLGGAPLGLRLPRETDEE
 PEEPGRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQTLNILVDTGSSNFA
 VGAAPHFPLHRYYQRQLSSTYRDLRKGVYEPYTQGKWEGEGLGTDLVSIPH
 GPNVTVRANIAAITESEDKFFINGSNWEGLAYAEIARPDDSLFPFFDS
 LVKQTHVPNLFLSQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGS LW
 YTPIRREWYYEVIIVRVEINGQDLKMDCKE NYDKSIVDSGTTNLRLPKK
 VFEAAVKSIAASSTEKF PDGFWLGEQLVCWQAGTPWNIFPVISLYLMG
 EVTNQSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIME
 GFYVVFDRARKRIGFAVSACHVDEFRTAAVEGPFTLDMEDCGYNIPQT
 K
 DESTLMTIAYVMAAICALFMLPLCLMVCQWRCLRCLRQQHDDFADDISLL

>2

MAQALPWLLLWMGAGVLP AHLTQH GIRLPLRSGLGGAPLGLRLPRETDEE
 PEEPGRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQTLNILVDTGSSNFA
 VGAAPHFPLHRYYQRQLSSTYRDLRKGVYEPYTQGKWEGEGLGTDLVSIPH
 GPNVTVRANIAAITESEDKFFINGSNWEGLAYAEIARPDDSLFPFFDS
 LVKQTHVPNLFLSQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGS LW
 YTPIRREWYYEVIIVRVEINGQDLKMDCKE NYDKSIVDSGTTNLRLPKK
 VFEAAVKSIAASSTEKF PDGFWLGEQLVCWQAGTPWNIFPVISLYLMG
 EVTNQSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIME
 GFYVVFDRARKRIGFAVSACHVDEFRTAAVEGPFTLDMEDCGYNIPQT
 K
 DESTLMTIAYVMAAICALFMLPLCLMVCQWRCLRCLRQQHDDFADDISLL